SEQUENCE LISTING

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<120> Modification of Feeding Behavior Using PYY and GLP-1

<130> 4040.001000

<150> PCT/GB03/00062
<151> 2003-01-10

<150> PCT/US02/31944

<151> 2002-09-24

<150> 60/392,109
<151> 2002-06-28

<150> GB 0200507.2
<151> 2002-01-10

<160> 341

<170> PatentIn version 3.1

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Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 3
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Ala Ser Leu Glu Pro Glu Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

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1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
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<400> 6

Tyr Pro Ala Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
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<213> Cavia porcellus

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Tyr Pro Ser Lys Pro Glu Ala Pro Gly Ser Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ala Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

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<213> Rana sp.

<400> 8

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Met Thr Lys Tyr Leu Thr Ala Leu Arg His Tyr Ile Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

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<212> PRT
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Tyr Pro Pro Lys Pro Glu Asn Pro Gly Asp Asp Ala Ala Pro Glu Glu
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            20                  25                  30

Arg Gln Arg Tyr
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            20                  25                  30

Arg Gln Arg Tyr
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Phe Pro Pro Lys Pro Asp Asn Pro Gly Asp Asn Ala Ser Pro Glu Gln
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Met Ala Arg Tyr Lys Ala Ala Val Arg His Tyr Ile Asn Leu Ile Thr
            20                  25                  30

Arg Gln Arg Tyr
        35
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<213> Petromyzontidae gen. sp.

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Leu Ser Lys Tyr Met Leu Ala Val Arg Asn Tyr Ile Asn Leu Ile Thr
            20                  25                  30
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Arg Gln Arg Tyr
35

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
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Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
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Arg Gln Arg Tyr
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<400> 16

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Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

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<213> Bos taurus

<400> 17

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

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<213> Ovis aries

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Asp Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

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1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
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<213> Avian

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Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
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Met Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
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<213> Carassius auratus

<400> 22

Tyr Pro Thr Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Glu
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

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Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Asp
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Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

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<213> Lampetra sp.

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Pro Pro Asn Lys Pro Asp Ser Pro Gly Glu Asp Ala Pro Ala Glu Asp
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Leu Ala Arg Tyr Leu Ser Ala Val Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
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Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
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Met Ala Gln Tyr Ala Ala Asp Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
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Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln
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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

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<213> Canis familiaris

<400> 27

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln
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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
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<213> Felis catus

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Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

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<213> Bos taurus

<400> 29

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Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
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Arg Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr
20 25 30

Arg Pro Arg Tyr
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<400> 31

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Met Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr
20 25 30

Arg Pro Arg Tyr
35

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<400> 32

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
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Gln Met Ala Gln Tyr Ala Ala Glu Met Arg Arg Tyr Ile Asn Met Leu
20 25 30

Thr Arg Pro Arg Tyr
35

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<213> Gallus gallus

<400> 33

Gly Pro Ser Gln Pro Thr Tyr Pro Gly Asp Asp Ala Pro Val Glu Asp
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Leu Ile Arg Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr
20 25 30

Arg His Arg Tyr
35

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Thr Pro Leu Gln Pro Lys Tyr Pro Gly Asp Gly Ala Pro Val Glu Asp
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Leu Ile Gln Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr
20 25 30

Arg Pro Arg Phe
35

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<213> Rana catesbeiana

<400> 35

Ala Pro Ser Glu Pro His His Pro Gly Asp Gln Ala Thr Pro Asp Gln
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Leu Ala Gln Tyr Tyr Ser Asp Leu Tyr Gln Tyr Ile Thr Phe Ile Thr
20 25 30

Arg Pro Arg Phe
35

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Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr
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<400> 38

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
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Arg His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

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Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Tyr
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1 5 10

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1 5 10

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Lys His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr
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Lys His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr
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Lys His Tyr Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

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1 5 10

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1 5 10

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1 5 10

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Lys His Tyr Leu Asn Leu Val Thr Arg Gln Lys Tyr

1 5 10

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Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Phe
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Arg His Thr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

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Arg His Thr Leu Gln Leu Val Thr Arg Gln Arg Tyr
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1 5 10

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Arg His Thr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
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<400> 82

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<400> 84

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1 5 10

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<400> 87

Arg His Phe Leu Asn Leu Val Ser Arg Gln Arg Tyr
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<400> 88

Arg His Phe Leu Asn Leu Val Thr Lys Gln Arg Tyr
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Arg His Tyr Leu Gln Ile Val Thr Arg Gln Arg Tyr
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Arg His Tyr Leu Gln Leu Val Ser Arg Gln Arg Tyr
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Arg His Tyr Leu Gln Leu Val Thr Lys Gln Arg Tyr
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Arg His Tyr Leu Gln Leu Val Thr Arg Asn Arg Tyr
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<400> 100

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Lys Tyr
1 5 10

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<400> 101

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Thr
1 5 10

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<400> 102

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Phe
1 5 10

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<400> 103

Arg His Tyr Leu Asn Ile Ile Thr Arg Gln Arg Tyr
1 5 10

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<400> 104

Arg His Tyr Leu Asn Ile Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 105
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<220>
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<400> 105

Arg His Tyr Leu Asn Ile Val Ser Arg Gln Arg Tyr
1 5 10

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<400> 106

Arg His Tyr Leu Asn Ile Val Thr Lys Gln Arg Tyr
1 5 10

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<400> 107

Arg His Tyr Leu Asn Ile Val Thr Arg Asn Arg Tyr
1 5 10

<210> 108
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<220>
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<400> 108

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Lys Tyr
1 5 10

<210> 109
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<400> 109

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Thr
1 5 10

<210> 110
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<400> 110

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Phe
1 5 10

<210> 111
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<400> 111
Arg His Tyr Leu Asn Val Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 112
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<400> 112

Arg His Tyr Leu Asn Val Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 113
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<400> 113

Arg His Tyr Leu Asn Val Val Ser Arg Gln Arg Tyr

1 5 10

<210> 114
<211> 12
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<220>
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<400> 114

Arg His Tyr Leu Asn Val Val Thr Lys Gln Arg Tyr
1 5 10

<210> 115
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<400> 115

Arg His Tyr Leu Asn Val Val Thr Arg Asn Arg Tyr
1 5 10

<210> 116
<211> 12
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<220>
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<400> 116

Arg His Tyr Leu Asn Val Val Thr Arg Gln Lys Tyr
1 5 10

<210> 117
<211> 12
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<400> 117

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Thr
1 5 10

<210> 118
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<400> 118

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Phe
1 5 10

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<400> 119

Arg His Tyr Leu Asn Leu Ile Ser Arg Gln Arg Tyr
1 5 10

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<400> 120

Arg His Tyr Leu Asn Leu Ile Thr Lys Gln Arg Tyr
1 5 10

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<400> 121

Arg His Tyr Leu Asn Leu Ile Thr Arg Asn Arg Tyr
1 5 10

<210> 122
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<400> 122

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Lys Tyr
1 5 10

<210> 123
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<400> 123

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Thr
1 5 10

<210> 124
<211> 12
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<400> 124

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Phe
1 5 10

<210> 125
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<400> 125

Arg His Tyr Leu Asn Leu Leu Ser Arg Gln Arg Tyr
1 5 10

<210> 126
<211> 12
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<220>
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<400> 126

Arg His Tyr Leu Asn Leu Leu Thr Lys Gln Arg Tyr
1 5 10

<210> 127
<211> 12
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<400> 127

Arg His Tyr Leu Asn Leu Leu Thr Arg Asn Arg Tyr
1 5 10

<210> 128
<211> 12
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<400> 128

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Lys Tyr
1 5 10

<210> 129
<211> 12
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<400> 129

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Thr
1 5 10

<210> 130

<211> 12
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<220>
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<400> 130

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Phe
1 5 10

<210> 131
<211> 12
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<220>
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<400> 131

Arg His Tyr Leu Asn Leu Val Ser Lys Gln Arg Tyr
1 5 10

<210> 132
<211> 12
<212> PRT
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<220>
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<400> 132

Arg His Tyr Leu Asn Leu Val Ser Arg Asn Arg Tyr
1 5 10

<210> 133
<211> 12
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<213> Artificial Sequence

<220>
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<400> 133

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Lys Tyr
1 5 10

<210> 134
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<212> PRT
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<220>
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<400> 134

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Thr
1 5 10

<210> 135
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<220>
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<400> 135

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 136
<211> 12
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<213> Artificial Sequence

<220>
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<400> 136

Arg His Tyr Leu Asn Leu Val Thr Lys Asn Arg Tyr
1 5 10

<210> 137
<211> 12
<212> PRT
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<220>
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<400> 137

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Lys Tyr
1 5 10

<210> 138
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
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<400> 138

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Thr
1 5 10

<210> 139
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 139

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Phe
1 5 10

<210> 140
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 140

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Lys Tyr
1 5 10

<210> 141
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 141

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Thr
1 5 10

<210> 142
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
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<400> 142

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Phe
1 5 10

<210> 143
<211> 12
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<220>
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<400> 143

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Thr
1 5 10

<210> 144
<211> 12
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<220>
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<400> 144

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Phe
1 5 10

<210> 145
<211> 13
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<220>

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<400> 145

Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 146
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<400> 146
Ile Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 147
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 147

Val Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 148
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 148

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 149
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 149

Thr Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 150
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<400> 150

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 151
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 151

Ser Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 152
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 152

Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 153
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 153

Thr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 154
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 154

Phe Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 155

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 156
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 156

Thr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 157
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 157

Phe Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 158
<211> 18

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 158

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 159
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 159

Lys Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 160
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 160

Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 161
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 161

Gln Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 162
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 162

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 163
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 163

Ile Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 164
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 164

Val Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 165
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 165

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 166
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 166

Asp Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 167
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 167

Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 168
<211> 22
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<400> 168

Asp Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 169
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 169

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
20

<210> 170
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 170

Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 171
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 171

Thr Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 172
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 172

Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 173
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 173

Ser Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 174
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 174

Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 175

<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 175

Glu Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 176
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 176

Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg
1 5 10 15

His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 177
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 177

Asp Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg
1 5 10 15

His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 178
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 178

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu
1 5 10 15

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 179
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 179

Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1 5 10 15

Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 180
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 180

Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 181
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 181

Ser Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 182
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 182

Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr
1 5 10 15

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 183
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 183

Asp Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr
1 5 10 15

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 184
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 184

Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
1 5 10 15

Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 185
<211> 33

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 185

Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 186
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 186

Arg Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 187
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 187

Gln Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 188
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 188

Asn Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 189
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 189

Leu Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 190
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 190

Val Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 191
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 191

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 192
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 192

Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 193
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 193

Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 194
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 194

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 195
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 195

Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 196
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 196

Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 197
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 197

Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 198
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 198

Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 199
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 199

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 200
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 200

Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 201
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 201

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr

20

<210> 202
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 202

Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
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<210> 203
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 203

Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 204
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 204

Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 205
<211> 26
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 205

Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 206
<211> 28
<212> PRT
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<220>
<223> Polypeptide variation

<400> 206

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu
1 5 10 15

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 207
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 207

Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1 5 10 15

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 208
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 208

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Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1               5                   10                  15

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
            20                  25
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<210> 209
<211> 30
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<220>
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<400> 209

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Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala
1               5                   10                  15

Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
            20                  25                  30
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<210> 210
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 210

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Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
1               5                   10                  15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
            20                  25                  30
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<210> 211
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 211

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Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr
1               5                   10                  15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
            20                  25                  30
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<210> 212
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 212

Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg

20 25 30

Tyr

<210> 213
<211> 13
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<220>
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<220>
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<400> 213

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 214
<211> 13
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<220>
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<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<400> 214

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr

1 5 10

<210> 215
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 215

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 216
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 216

Pro Ala Glu Asp Leu Ala Gln Tyr Ala Ala Glu Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Leu Thr Arg Gln Arg Tyr
20

<210> 217
<211> 20
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<220>
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<222> (20)..(20)
<223> AMIDATION

<400> 217

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
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<210> 218
<211> 20
<212> PRT
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<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 218

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 219
<211> 19
<212> PRT
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<220>
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<223> AMIDATION

<400> 219

Ala Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 220
<211> 20
<212> PRT
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<220>
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<220>
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<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 220

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 221
<211> 18
<212> PRT
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<220>
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<222> (18)..(18)
<223> AMIDATION

<400> 221

Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 222
<211> 20
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<220>
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<222> (20)..(20)
<223> AMIDATION

<400> 222

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 223
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<223> AMIDATION

<400> 223

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 224
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<212> PRT
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<220>
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<222> (20)..(20)
<223> AMIDATION

<400> 224

Ala Ala Arg Tyr Ser His Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 225
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<220>
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<222> (19)..(19)
<223> AMIDATION

<400> 225

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 226
<211> 20
<212> PRT
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<223> AMIDATION

<220>
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<222> (1)..(1)
<223> ACETYLATION

<400> 226

Arg Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 227
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<400> 227

Gln Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
1 5 10 15

Arg Tyr

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<220>
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<223> AMIDATION

<400> 228

Ala Arg Phe Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 229
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<212> PRT
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<222> (20)..(20)
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<400> 229

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 230
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<400> 230

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 231
<211> 20
<212> PRT
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<220>
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<222> (19)..(19)
<223> AMIDATION

<400> 231

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 232
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<400> 232

Ala Arg Tyr Tyr Ser Glu Leu Arg Arg Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 233
<211> 20
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<222> (20)..(20)
<223> AMIDATION

<400> 233

Xaa Ala Arg Tyr Ala Ser Ala Leu Arg His Tyr Leu Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 234
<211> 19
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<400> 234

Ala Arg Tyr Tyr Thr Gln Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 235
<211> 20
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<222> (20)..(20)
<223> AMIDATION

<400> 235

Leu Ala Arg Tyr Tyr Ser Asn Leu Arg His Tyr Ile Asn Val Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 236
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<223> AMIDATION

<400> 236

Ala Arg Tyr Tyr Asp Ser Leu Arg His Tyr Ile Asn Thr Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 237
<211> 19
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<400> 237

Ala Arg Tyr Tyr Ser Ala Leu Gln His Tyr Ile Asn Leu Leu Thr Arg
1 5 10 15

Pro Arg Tyr

<210> 238
<211> 20
<212> PRT
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<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 238

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg Gln Tyr Arg Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Phe
20

<210> 239
<211> 18
<212> PRT
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<222> (18)..(18)
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<400> 239

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln

1 5 10 15

Arg Phe

<210> 240
<211> 19
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<222> (19)..(19)
<223> AMIDATION

<400> 240

Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 241
<211> 19
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<220>
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<400> 241

Ser Arg Tyr Tyr Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 242
<211> 20
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<222> (20)..(20)
<223> AMIDATION

<400> 242

Xaa Ala Arg Tyr Tyr Asn Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 243
<211> 19
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<400> 243

Xaa Arg Tyr Glu Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

His Arg Tyr

<210> 244
<211> 21
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<222> (1)..(1)
<223> Bz

<400> 244

Xaa Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile
1 5 10 15

Thr Arg Pro Arg Phe
20

<210> 245
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<222> (19)..(19)
<223> AMIDATION

<400> 245

Ala Leu Tyr Tyr Ser Ala Leu Arg His Phe Val Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 246
<211> 19
<212> PRT
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<220>
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<223> AMIDATION

<400> 246

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Val Asn Leu Ile Phe Arg
1 5 10 15

Gln Arg Tyr

<210> 247
<211> 18
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<223> MeSer

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<222> (18)..(18)
<223> AMIDATION

<400> 247

Xaa Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Met Ile Thr Arg Gln
1 5 10 15

Arg Phe

<210> 248
<211> 20
<212> PRT
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<400> 248

Arg Ile Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Phe
20

<210> 249
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<222> (20)..(20)
<223> AMIDATION

<400> 249

Leu Ser Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 250
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<223> Xaa is MeIle

<400> 250

Xaa Arg Tyr Tyr Ser Ala Leu Gln His Phe Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 251
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<220>
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<222> (19)..(19)
<223> AMIDATION

<400> 251

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Phe

<210> 252
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<222> (20)..(20)
<223> AMIDATION

<400> 252

Met Ala Arg Tyr Tyr Ser Asp Leu Arg Arg Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 253
<211> 19
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<220>
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<222> (19)..(19)
<223> AMIDATION

<400> 253

Ala Arg Tyr Tyr Ser Glu Leu Arg His Tyr Ile Ile Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 254
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<212> PRT
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<220>
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<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 254

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 255
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 255

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 256
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<220>
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<222> (35)..(35)
<223> AMIDATION

<400> 256

Tyr Pro Ala Lys Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu
1 5 10 15

Ser Thr Tyr Tyr Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg
20 25 30

Glx Arg Tyr
35

<210> 257
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<220>
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<222> (15)..(15)
<223> AMIDATION

<400> 257

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 258
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<220>
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<222> (15)..(15)
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<400> 258

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr
1 5 10 15

<210> 259
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation
<220>
<221> MOD_RES

<222> (15)..(15)
<223> AMIDATION

<400> 259

Ala Ala Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr
1 5 10 15

<210> 260
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 260

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 261
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 261

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Xaa Arg Tyr
1 5 10 15

<210> 262
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is p.Cl.Pro; 4 chlorophenylalanine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 262

Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 263
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 263

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 264
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<400> 264

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Gln Arg Xaa
1 5 10 15

<210> 265
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
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<222> (13)..(13)
<223> Xaa is Ornithine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<400> 265

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Xaa Arg Xaa
1 5 10 15

<210> 266
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<220>
<221> LIPID
<222> (1)..(1)
<223> N alpha myristoyl

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 266

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 267
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N alpha naphthateneacetyl

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 267

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<400> 268

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Xaa Arg Xaa
1 5 10 15

<210> 269
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 269

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 270
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<220>
<221> MOD_RES
<222> (7)..(7)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<400> 270

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 271
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is 4,4' biphenylalanine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<400> 271

Xaa Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 272
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<400> 272

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 273
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<400> 273

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 274
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 274

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 275
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 275

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 276
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 2 thienylalanine

<400> 276

Ala Ser Leu Arg Asn Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 277
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is tetrahydroisoquinoline

<400> 277

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 278
<211> 3
<212> PRT
<213> Homo sapiens

<400> 278

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<210> 279
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> AMIDATION

<400> 279

His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 280
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is 2 thienylalanine

<400> 280

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Xaa
1 5 10 15

<210> 281
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
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<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 4 Thiazolylalanine

<400> 281

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 282
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 4 Thiazolylalanine

<400> 282

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 283
<211> 3

<212> PRT
<213> Homo sapiens

<400> 283

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<210> 284
<211> 3
<212> PRT
<213> Homo sapiens

<400> 284

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<210> 285
<211> 3
<212> PRT
<213> Homo sapiens

<400> 285

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<210> 286
<211> 3
<212> PRT
<213> Homo sapiens

<400> 286

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<210> 287
<211> 3
<212> PRT
<213> Homo sapiens

<400> 287

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<210> 288
<211> 3
<212> PRT

<213> Homo sapiens

<400> 288

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<210> 289
<211> 15
<212> PRT
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<220>
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<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 289

Phe Ser Leu Arg Asn Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 290
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 290

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 291

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 291

Ala Ser Leu Arg His Tyr Trp Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 292
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 292

Ala Ser Leu Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 293
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
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<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 293

Ala Ser Leu Arg Ala Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 294
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (14)..(14)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is 3' benzothienyalanine

<400> 294

Ala Ser Leu Arg Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 295
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>

<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 295

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 296
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 296

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10 15

<210> 297
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is D form of Trp

<220>
<221> MOD_RES
<222> (11)..(11)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N alpha ACETYLATION

<400> 297

Ala Ser Leu Arg His Phe Leu Asn Leu Val Xaa Arg Gln Arg Tyr
1 5 10 15

<210> 298
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to CH3CO

<400> 298

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 299
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to CH3CO

<400> 299

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 300
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<400> 300

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 301
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<400> 301

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 302
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
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<222> (7)..(7)
<223> Xaa is Norleucine

<220>
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<222> (9)..(9)
<223> Xaa is Norleucine

<400> 302

Ala Ser Xaa Arg His Trp Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 303
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES

<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
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<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
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<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
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<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 303

Ala Ser Xaa Arg His Trp Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 304
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
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<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
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<220>
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<223> Xaa is Norleucine

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<223> Xaa is Norleucine

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<222> (9)..(9)
<223> Xaa is Norleucine

<220>
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<222> (10)..(10)
<223> Xaa is Norvaline

<400> 304

Ala Ser Xaa Arg His Phe Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 305
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
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<220>
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<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
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<222> (14)..(14)

<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 305

Ala Ser Xaa Arg His Phe Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 306
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<400> 306

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Xaa Xaa
1 5 10

<210> 307
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
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<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<400> 307

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr
1 5 10

<210> 308
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
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<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a psuedopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a psuedopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 308

Ala Ser Leu Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 309
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 309

Ala Ser Xaa Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa

1 5 10 15

<210> 310
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> bonded to OCH3

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<400> 310

Ile Asn Pro Ile Tyr Arg Leu Arg Tyr
1 5

<210> 311
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> DISULFID
<222> (4)..(4)
<223> Sequence is linked to identical sequence by a disulfide bond

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> C terminus is bonded to NH2

<400> 311

Ile Asn Pro Cys Tyr Arg Leu Arg Tyr
1 5

<210> 312

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> C terminus is bonded to OCH3

<220>
<221> DISULFID
<222> (1)..(1)
<223> sequence is linked to an identical sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<400> 312

Cys Tyr Arg Leu Arg Tyr
1 5

<210> 313
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Connected by NH CH CO

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Identical peptide chains are connected by (CH2)4 at the CH o
f NH CH CO

<400> 313

Ile Asn Pro Tyr Arg Leu Arg Tyr
1 5

<210> 314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> C terminus is bonded to OCH3

<400> 314

Tyr Arg Leu Arg Tyr Tyr Arg Leu Arg Tyr
1 5 10

<210> 315
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> DISULFID
<222> (18)..(22)
<223>

<400> 315

Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala
1 5 10 15

Arg Cys Tyr Ser Ala Cys Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
20 25 30

Arg Tyr

<210> 316
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 316

Arg His Tyr Leu Asn Leu Ile Gly Arg Gln Arg Tyr
1 5 10

<210> 317
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (3)..(7)
<223> ACETYLATION

<400> 317

Arg His Gly Leu Asn Leu Leu Gly Arg Gln Arg Tyr
1 5 10

<210> 318
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 318

Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 319
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 319

His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 320
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 320

Arg His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 321
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 321

Tyr Ile Asn Leu Leu Tyr Arg Gln Arg Tyr
1 5 10

<210> 322
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is 6 amino hexanoic acid

<400> 322

Tyr Pro Ser Leu Xaa Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10 15

<210> 323
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 323

Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5

<210> 324
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<400> 324

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 325
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 325

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 326
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminal is bonded to H

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 326

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 327
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (9)..(9)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<400> 327

Ala Ser Leu Arg Thr Arg Gln Arg Tyr
1 5

<210> 328
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MISC_FEATURE

<222> (6)..(6)
<223> Xaa is 2 thienylalanine

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 328

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 329
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 329

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 330
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 330

Asp Asp Asp Asp Tyr
1 5

<210> 331
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 331

Gly Pro Arg
1

<210> 332
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 332

Ala Gly Gly
1

<210> 333
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 333

His Pro Phe His Leu
1 5

<210> 334
<211> 34
<212> PRT

<213> Homo sapiens

<400> 334

Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 335
<211> 34
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 335

Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala
1 5 10 15

Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
20 25 30

Arg Tyr

<210> 336
<211> 37
<212> PRT
<213> Homo sapiens

<400> 336

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val
1 5 10 15

Ser Ser Tyr Leu Glu Gly Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu
20 25 30

Val Lys Gly Arg Gly
35

<210> 337
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (36)..(36)
<223> C terminus is bonded to NH2

<400> 337

His Asp Glu Phe Glu Arg His Ala Glu Gly Thr Phe Thr Ser Asp Val
1 5 10 15

Ser Ser Tyr Leu Glu Gly Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu
20 25 30

Val Lys Gly Arg
35

<210> 338

<211> 31
<212> PRT
<213> Homo sapiens

<400> 338

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
20 25 30

<210> 339
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (30)..(30)
<223> C terminus is bonded to NH2

<400> 339

His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
1 5 10 15

Gly Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
20 25 30

<210> 340
<211> 37
<212> PRT
<213> Homo sapiens

<400> 340

His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Ser
1 5 10 15

Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asp Thr Lys Arg Asn
20 25 30

Lys Asn Asn Ile Ala
35

<210> 341 <211> 463 <212> PRT <213> homo sapiens <400> 341

Met Ala Gly Ala Pro Gly Pro Leu Arg Leu Ala Leu Leu Leu Leu Gly
1 5 10 15

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Met Val Gly Arg Ala Gly Pro Arg Pro Gln Gly Ala Thr Val Ser Leu
            20                  25                  30

Trp Glu Thr Val Gln Lys Trp Arg Glu Tyr Arg Arg Gln Cys Gln Arg
        35                  40                  45

Ser Leu Thr Glu Asp Pro Pro Pro Ala Thr Asp Leu Phe Cys Asn Arg
    50                  55                  60

Thr Phe Asp Glu Tyr Ala Cys Trp Pro Asp Gly Glu Pro Gly Ser Phe
65                  70                  75                  80

Val Asn Val Ser Cys Pro Trp Tyr Leu Pro Trp Ala Ser Ser Val Pro
                85                  90                  95

Gln Gly His Val Tyr Arg Phe Cys Thr Ala Glu Gly Leu Trp Leu Gln
            100                 105                 110

Lys Asp Asn Ser Ser Leu Pro Trp Arg Asp Leu Ser Glu Cys Glu Glu
        115                 120                 125

Ser Lys Arg Gly Glu Arg Ser Ser Pro Glu Glu Gln Leu Leu Phe Leu
    130                 135                 140

Tyr Ile Ile Tyr Thr Val Gly Tyr Ala Leu Ser Phe Ser Ala Leu Val
145                 150                 155                 160

Ile Ala Ser Ala Ile Leu Leu Gly Phe Arg His Leu His Cys Thr Arg
                165                 170                 175

Asn Tyr Ile His Leu Asn Leu Phe Ala Ser Phe Ile Leu Arg Ala Leu
            180                 185                 190

Ser Val Phe Ile Lys Asp Ala Ala Leu Lys Trp Met Tyr Ser Thr Ala
        195                 200                 205

Ala Gln Gln His Gln Trp Asp Gly Leu Leu Ser Tyr Gln Asp Ser Leu
    210                 215                 220

Ser Cys Arg Leu Val Phe Leu Leu Met Gln Tyr Cys Val Ala Ala Asn
225                 230                 235                 240
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Tyr Tyr Trp Leu Leu Val Glu Gly Val Tyr Leu Tyr Thr Leu Leu Ala
                245                 250                 255

Phe Ser Val Phe Ser Glu Gln Trp Ile Phe Arg Leu Tyr Val Ser Ile
            260                 265                 270

Gly Trp Gly Val Pro Leu Leu Phe Val Val Pro Trp Gly Ile Val Lys
        275                 280                 285

Tyr Leu Tyr Glu Asp Glu Gly Cys Trp Thr Arg Asn Ser Asn Met Asn
    290                 295                 300

Tyr Trp Leu Ile Ile Arg Leu Pro Ile Leu Phe Ala Ile Gly Val Asn
305                 310                 315                 320

Phe Leu Ile Phe Val Arg Val Ile Cys Ile Val Val Ser Lys Leu Lys
                325                 330                 335

Ala Asn Leu Met Cys Lys Thr Asp Ile Lys Cys Arg Leu Ala Lys Ser
            340                 345                 350

Thr Leu Thr Leu Ile Pro Leu Leu Gly Thr His Glu Val Ile Phe Ala
        355                 360                 365

Phe Val Met Asp Glu His Ala Arg Gly Thr Leu Arg Phe Ile Lys Leu
    370                 375                 380

Phe Thr Glu Leu Ser Phe Thr Ser Phe Gln Gly Leu Met Val Ala Ile
385                 390                 395                 400

Leu Tyr Cys Phe Val Asn Asn Glu Val Gln Leu Glu Phe Arg Lys Ser
                405                 410                 415

Trp Glu Arg Trp Arg Leu Glu His Leu His Ile Gln Arg Asp Ser Ser
            420                 425                 430

Met Lys Pro Leu Lys Cys Pro Thr Ser Ser Leu Ser Ser Gly Ala Thr
        435                 440                 445

Ala Gly Ser Ser Met Tyr Thr Ala Thr Cys Gln Ala Ser Cys Ser
    450                 455                 460
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